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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/644,084	08/20/2003	Yoshimi Takai	2144.0100000/RWE/ALS	4948

26111 7590 04/19/2007

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EXAMINER	
BASI, NIRMAL SINGH	
ART UNIT	PAPER NUMBER
1646	

SHORTENED STATUTORY PERIOD OF RESPONSE	MAIL DATE	DELIVERY MODE
3 MONTHS	04/19/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

If NO period for reply is specified above, the maximum statutory period will apply and will expire 6 MONTHS from the mailing date of this communication.

Office Action Summary	Application No.	Applicant(s)	
	10/644,084	TAKAI ET AL.	
	Examiner	Art Unit	
	Nirmal S. Basi	1646	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *24 January 2007*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-15 and 19-23* is/are pending in the application.

4a) Of the above claim(s) *2,7-13 and 19-22* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1,3-6,14,15 and 23* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *22 December 2006* is/are: a)☐ accepted or b)☒ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☒ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *10/6/05*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

1. Amendment filed 1/24/07 has been entered. Applicant has amended claims 1, 4, 6, and added new claim 23. Claims 1 3-6, 14-15 and 23 are being examined as being directed to the elected invention. Claims 2, 7-13, 16-22 are either withdrawn or cancelled. Examiner rejections are recast below to address the amended claims. Applicants arguments have been fully considered but are not deemed persuasive to overcome the rejection of the amended claims as discussed below.

2. IDS filed 10/6/05 was considered on 8/15/06 but references AS22, AT22 and AR23 were not initialed. This was an oversight by the Examiner and references AS22, AT22 and AR23 have now been initialed as being considered and are attached with this Office action. References AR9, AR19 have been initialed again just to remove any ambiguity as to if they were considered or not.

3. The drawings remain objected to because Figure 2B is too dark and the figure is not legible. Applicants have filed new drawing on 12/22/06. Figure 2B is completely black and shows no data. Appropriate correction is required.

New corrected drawings in compliance with 37 CFR 1.121(d) are required in this application for the reasons given above. Applicant is advised to employ the services of a competent patent draftsperson outside the Office, as the U.S. Patent and Trademark Office no longer prepares new drawings. The corrected drawings are required in reply to the Office action to avoid abandonment of the application. The requirement for corrected drawings will not be held in abeyance.

4. a) The amendment filed 12/28/06 is objected to because it does not include the statement "the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing" and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b) or 1.825(d). A statement that the sequence listing information is identical is required. Further to replace the existing sequence with that filed 12/28/06 a statement to that effect is required.

b) A partial copy of the sequence listing on the CRF is attached. The CRF contained errors which were corrected by STIC, see attached "RAW SEQUENCE LISTING" (Appendix 1).

Claim Rejections - 35 USC § 112, second paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

5. Claims 1, 3 -6, 14-15 and 23 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim is indefinite because of the use of the phrase "nucleotide sequence corresponding to". It is suggested to overcome the rejection Applicants amend the claim to "nucleotide sequence set forth at". Further, claim I is indefinite because it is not clear how the polynucleotide binds afadin or actinin. It is suggested to overcome the rejections the claim be amended as follows:

1. An isolated and purified_polynucleotide selected from the group consisting of:
(a) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO: 2;

(b) a polynucleotide comprising the nucleotide sequence set forth at ~~of corresponding to~~ position 80 to 1924 in SEQ ID NO:1; and

(c) a polynucleotide comprising the nucleotide sequence with at least 95% homology to the nucleotide sequence set forth at ~~corresponding to~~ position 80 to 1924 in SEQ ID NO: 1, wherein the polynucleotide encodes a polypeptide which binds ~~which have the binding activity to~~ afadin and/or actinin.

Claim 6 is rejected because it is broader in scope than the base claim from which it depends.

Claims 3 -5, 14-15 and 23 are rejected for depending on an indefinite base claim and fail to resolve the issued raised above.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

6. Claim 6 is rejected under 35 U.S.C. 1 12, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant ad that the inventors), at the time the application was filed, had possession of the claimed invention. The claim is drawn to:

An isolated and purified polynucleotide, which comprises at least 15

nucleotides of claim 1.

The claims, as written, encompass polynucleotides, which vary substantially in length and also in nucleotide composition. The instant disclosure does not adequately describe the scope of the claimed genus, which has insufficient structural limitations to correspond to the functional limitations. The claims encompass a substantial variety of subgenera including derivatives, allelic variants, chimeric constructs, fusion constructs etc. which may not even contain the critical structural feature of the invention contained in the afadin, actininα or actininβ binding domain of ADIP.

The specification discloses a polynucleotide (SEQ ID NO:1) encoding a polypeptide (SEQ ID NO:2) which binds afadin, α–actinin-1 or α–actinin-2, wherein the polypeptide comprises the afadin, actininα or actininβ binding domain disclosed in Figure 3A. The specification also discloses truncated polynucleotide of SEQ ID NO:1 encoding truncated polypeptide SEQ ID NO:2 which binds afadin, α–actinin-1 or α–actinin-2, wherein the polynucleotide comprises the afadin, actininα or actininβ binding domain disclosed in Figure 3A. The specification is enabled for polynucleotide encoding polypeptide which bind afadin, α–actinin-1 or α–actinin-2, wherein the polypeptide comprises the afadin, actininα or actininβ binding domain disclosed in Figure 3A.

The critical feature of the invention as it relates structure to function is the afadin, actininα or actininβ binding domain disclosed in Figure 3A. The structure is the domain contained in the polypeptide of SEQ ID NO:1, and the function is that said domain binds afadin, actininα or actininβ. The structure has to be a

minimum length and composition. The critical feature of the invention as it relates to structure and function is not contained, for example, in a polynucleotide that is 15 nucleotides long as claimed in claim 6.

To provide evidence of possession of a claimed genus, the specification must provide sufficient distinguishing identifying characteristics of the genus. The factors to be considered include disclosure of compete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, methods of making the claimed product, or any combination thereof. As cited above many polynucleotide constructs, which combine specific structure to function, are enabled by the disclosure, the claims that do not, as indicted above, are not enabled.

Pertaining to the claim 6 there is no identification of any particular portion of the structure of the peptide of SEQ ID NO:2 that must be conserved for activity. Accordingly, in the absence of sufficient recitation of distinguishing identifying characteristics, the specification does not provide adequate written description of the claimed genus. The structural limitations in the claim are insufficient to define the genus claimed, which encompasses unrelated peptides.

Naming a type of material generically known to exist, in the absence of knowledge as to what that material consists of, is not a description of that material. When one is unable to envision the detailed constitution of a complex chemical compound having a particular function, such as a peptide or nucleic acid, so as to distinguish it from other materials, as well as a method for obtaining it, conception has not been achieved until reduction to practice has

occurred, i.e., until after the peptide or nucleic acid has been isolated. Thus, claiming all peptides or DNAs that achieve a result without defining what means will do so is not in compliance with the description requirement. Rather, it is an attempt to preempt the future before it has arrived. The claims recite a broad arbitrary structural relationship between the claimed polynucleotide sequence and the disclosed polynucleotide of SEQ ID NO:1. Therefore, unrelated peptides to SEQ ID NO:2 are encompassed by the claims.

Vas-Cath Inc. v. Mahurkar, 19USPQ2d 1111 , clearly states that applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of the invention. The invention is, for purposes of the 'written description" inquiry, whatever is now claimed." (See page 1117.) The specification does not "clearly allow persons of ordinary skill in the ad to recognize that (he or she) invented what is claimed." (See *Vas-Cath* at page 1116). As discussed above, the skilled artisan cannot envision the detailed chemical structure of the encompassed genus of peptide, and therefore conception is not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method of isolating it. The compound itself is required. See *Fiers v. Revel*, 25 USPQ2d 1601 at 1606 (CAFC1993) and *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ2d 1016.

One cannot describe what one has not conceived. See *Fiddes v. Baird,* 30 USPQ2d 1481 at 1483. In *Fiddes*, claims directed to mammalian FGF'S were

found to be unpatentable due to lack of written description for that broad class. The specification provided only the bovine sequence.

Therefore, only isolated polynucleotide of SEQ ID NO:1 encoding the amino acid sequence set forth in SEQ ID NO:2 but not the full breadth of the claims meets the written description provision of 35 U.S.C.112, first paragraph. Applicant is reminded that Vas-Cath makes clear that the written description provision of 35 U.S.C. 112 is severable from its enablement provision (see page 1 115).

7. Claim 1, and dependent claims 3-6, 15 and 23 rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. The added material which is not supported by the original disclosure is as follows: A) An isolated and purified polynucleotide comprising the nucleotide sequence corresponding to **position 80 to 1924 in SEQ ID NO: 1.** B) An isolated and purified polynucleotide comprising the nucleotide sequence with **at least 95% homology** to the nucleotide sequence corresponding to **position 80 to 1924 in SEQ ID NO: 1** which have the binding activity to afadin and/or actinin

There is no support in the specification for the species of polynucleotide comprising the nucleotide sequence corresponding to **position 80 to 1924 in**

SEQ ID NO: 1. There is no support in the specification for the species of polynucleotide comprising the nucleotide sequence with **at least 95% homology** to the nucleotide sequence corresponding to **position 80 to 1924 in SEQ ID NO: 1** which have the binding activity to afadin and/or actinin.

Applicant is required to cancel the new matter in the reply to this Office Action or show support for such a construct.

8. Claim 6 is rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. The added material which is not supported by the original disclosure is as follows: A)

"An isolated and purified host cell **transformed** with the polynucleotide of claim 1". There is no support in the specification for the host cell **transformed** with the polynucleotide of claim 1.

Applicant is required to cancel the new matter in the reply to this Office Action or show support for such a construct.

9 If applicant overcomes the written description rejection above then claims 1, 3-6, 15 and 23 will be rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated and purified polynucleotide selected from the group consisting of: (a) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO: 2; (b) a polynucleotide

comprising the nucleotide sequence set forth at position 80 to 1924 in SEQ ID NO:1; and (c) a polynucleotide comprising the nucleotide sequence with at least 95% homology to the nucleotide sequence set forth at position 80 to 1924 in SEQ ID NO: 1, wherein the polynucleotide encodes a polypeptide which binds afadin and/or actinin;, vector comprising said polynucleotide, isolated host cell comprising said vector, method of using said cell to produce the enabled polypeptide of claim 1; and polynucleotide fragments of the polynucleotide of SEQ ID NO:1 which are of sufficient length to be used as specific hybridization probes to detect the polynucleotide encoding the polypeptide which binds afadin, actininα or actininβ, wherein the polypeptide comprises the afadin, α–actinin-1 or α–actinin-2 binding domain disclosed in Figure 3C, does not reasonably provide enablement for other polynucleotides. The, specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

Based on the disclosure a person of ordinary skill in the art would, in light of the specification, be able to isolate polynucleotide encoding a polypeptide which binds afadin, α–actinin-1 or α–actinin-2, comprising the afadin, α–actinin-1 or α–actinin-2 binding domain disclosed in Figure 3C. A person of ordinary skill in the art , in light of the specification, would also be able to produce vector comprising the enabled polynucleotide and host cell comprising said vector and use said host cell to produce the enabled polynucleotide of claim 1.

The scope of the claims, which encompass other polynucleotides

encoding polypeptides not comprising the afadin, actininα or actininβ binding domain disclosed in Figure 3C are not enabled by the disclosure. Further the scope of the claims, which encompass other polynucleotides encoding polypeptides comprising the afadin or actinin binding activity but structurally unrelated to the polynucleotide of SEQ ID NO:1 are not enabled by the disclosure. The specification, Figure 3A, discloses the critical structural regions of the polypeptide of SEQ ID NO:2 (ADIP) which is required for afadin, α–actinin-1 or α–actinin-2 binding. ADIP has been shown to bind afadin, α–actinin-1 or α–actinin-2. The claims encompass variant polynucleotides which may have as little a 15 nucleotides in common with the polynucleotide of SEQ ID NO:1 and none of the afadin, α–actinin-1 or α–actinin-2 binding. Applicant has not disclosed how to use said variants. Variant molecules which are structurally unrelated to ADIP are encompassed by the claims. Although these molecules may bind afadin, actinin they may have physiological functions unrelated to the ADIP of instant invention. Applicant has not disclosed how to use said variant molecules. For example, Applicant has not shown how to use variant polynucleotides comprising 15 nucleotides that hybridize to the polynucleotide of SEQ ID NO:1. Said variant polynucleotides comprising 15 nucleotides may be not even contain the critical feature of the invention as it relates structure to function.

Clearly, a single disclosed sequence does not support claims to any polynucleotide comprising 15 nucleotides of SEQ ID NO:1. Due to the large quantity of experimentation necessary to make and use the variant

polynucleotides of claimed invention lacking with the critical feature of the invention as it relates structure to function, the lack of direction/guidance presented in the specification regarding the identification, purification, isolation and characterization of said variant polynucleotides, the unpredictability of the effects of mutation on the structure and function of variant polynucleotides (since mutations of SEQ ID NO:1 and 2 are also encompassed by the claim), and the breadth of the claim which fail to recite meaningful structural and functional limitations, undue experimentation would be required of the skilled artisan to make or use the claimed invention in its full scope.

10 The rejections of record under 35 U.S.C. 112, first paragraph are maintained for reasons of record as they apply to the amended claims. Claims 1, 3-6, 15-18 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated polynucleotide encoding a polypeptide which binds afadin, α–actinin-1 or α–actinin-2, wherein the polypeptide comprises the afadin, actininα or actininβ binding domain disclosed in Figure 3A, vector comprising said polynucleotide, isolated host cell comprising said vector, method of using said cell to produce the enabled polypeptide of claim 1; and polynucleotide fragments of the polynucleotide of SEQ ID NO:1 which are of sufficient length to be used as specific hybridization probes to detect the polynucleotide encoding the polypeptide which binds afadin, actininα or actininβ, wherein the polypeptide comprises the afadin, α–actinin-1 or α–actinin-2 binding domain disclosed in Figure 3C, does not reasonably provide enablement

for other polynucleotides. The, specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

Based on the disclosure a person of ordinary skill in the art would, in light of the specification, be able to isolate polynucleotide encoding a polypeptide which binds afadin, α–actinin-1 or α–actinin-2, comprising the afadin, α–actinin-1 or α–actinin-2 binding domain disclosed in Figure 3C. A person of ordinary skill in the art , in light of the specification, would also be able to produce vector comprising the enabled polynucleotide and host cell comprising said vector and use said host cell to produce the enabled polynucleotide of claim 1. The rejection is the same as disclosed in the prior office Action.

Prior Art Rejections

Applicants argue the prior art references do not disclose the nucleotide sequence with at least 95% homology to the nucleotide sequence corresponding to position 80-1924 in SEQ ID NO:1. Applicant's arguments have been fully considered but they are not found persuasive. The following rejections are maintained. As seen by the sequence comparisons the polynucleotide sequence shown have at least 95% homology to the nucleotide sequence corresponding to position 80-1924 in SEQ ID NO:1..

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

11. Claims 1,3, 4, 6, 15-18 are rejected under 35 U.S.C. 102(b) as being anticipated by The RIKEN Genome Exploration Research group Phase II Team and the FANTOM Consortium (Nature, Vol. 409, pages 563-690, February 8, 2001)

The RIKEN Genome Exploration Research group Phase II Team and the FANTOM Consortium (Nature article, also see attached sequence comparison) disclose a polynucleotide, which has 99.4% query match and 99.9% identity to the polynucleotide of SEQ ID NO:1. Also disclosed are vector comprising said polynucleotide and cell comprising said vector. The disclosed polynucleotide encodes a polypeptide that inherently binds afadin and/or actinin, absent evidence to the contrary.

Therefore the disclosure of the RIKEN Genome Exploration Research group Phase II Team and the FANTOM Consortium meets the limitations of claims 1,3, 4, 6, 15-18, absent evidence to the contrary.

```
RESULT 1
AK043865
LOCUS       AK043865               3185 bp    mRNA    linear   HTC 02-SEP-2005
DEFINITION  Mus musculus 10 days neonate cortex cDNA, RIKEN full-length
            enriched library, clone:A830043F14 product:HYPOTHETICAL 71.0 KDA
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PROTEIN homolog [Mus musculus], full insert sequence.
ACCESSION AK043865
VERSION AK043865.1 GI:26335971
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6
AUTHORS RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the FANTOM Consortium.
TITLE Antisense Transcription in the Mammalian Transcriptome
JOURNAL Science 309, 1564-1566 (2005)
REFERENCE 7
AUTHORS The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).
TITLE The Transcriptional Landscape of the Mammalian Genome
JOURNAL Science 309, 1559-1563 (2005)
REFERENCE 8 (bases 1 to 3185)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,

```
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches 2689;  Conservative    0;  Mismatches    0;  Indels    3;  Gaps    1;

Qy          1 CGTAGGAGAGTGACAGGAGCTGTTGTAAGCGTCGCAGCACTGAGCCGCCTCCTCAGGTAT 60
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Db        370 CCTGGCTCTGGAACTTGCTATGGGAGATTGGATGACTGTGACAGATCCAGTTCTGTGTAC 429

Qy        121 AGAAAACAAAAATCTCTCTCAATATACCTCAGAAACAAAGATGTCTCCGTCCAGTTTGTA 180
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Qy        601 GAATGAGAAAGATGAGGTACAAAAATTACAAAATATCATAGCCAGCCGGGCTACTCAGTA 660
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Qy        661 TAATCATGATGTGAAGAGGAAGGAGCGTGAATATAATAAGCTAAAGGAGCGCCTGCATCA 720
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Qy        841 GATGTACAAAATTCTGTTGAATGATTATGAGTACCGCCAGAAGCAGATCCTGATGGAGAA 900
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Qy       1141 AGAAAAACTCGATAACCAAGCTTCGAAGGTACACTCAGAGGGCCTTAATGAGGAGGACGT 1200
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Qy       1261 TAAAGAGATGATCAAGGCTCAGCAGCAGCTCTTACAGCAGCAGCTGGCCACCACGTGTGA 1320
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Qy       1441 TACAGAAGCTGCCATTCGATTGGGGTTGGAGAGAAAGGCGTTTGAAGAAGAGCGAGCCAG 1500
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Qy       1561 GAAACTTTTCAGTGCCTTCTCAGGAAGTTCTGATCCAGACAATCTTATAGTCCACTCACG 1620
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Qy      1921 ACCTTAAATGTGCGGGCTGCAGTGCTGTTCCCAGATGTGCGCTAGAGGAGTTGACACAGG 1980
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Qy      1981 GTGTAGCATAAAGTCAGTCGTCTAACTTAAGATGCTCAGAGTTGTTTGTTTGGACTTCGC 2040
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Qy      2041 TGTCTTCCCCCAAAGAGCTGAAATGCTAAGCTACTTAAAAGGATGCAAAGCTTTGGTTGT 2100
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Db      2947 ATATGTGAATGTTATAATTTCTAAGAGGAATATTGATTATGGAGTAATGGGG 2998
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12. Claims 1,3, 4, 6, 15-18 are rejected under 35 U.S.C. 102(b) as being anticipated by Carninci et. al. (Genome Research, Vol. 10, pages 1617-1630, 2000)

Carninci et. al. (also see attached sequence comparison) disclose a polynucleotide, which has 99.4% query match and 99.9% identity to the polynucleotide of SEQ ID NO:1. Also disclosed are vector comprising said polynucleotide and cell comprising said vector. The disclosed polynucleotide encodes a polypeptide that inherently binds afadin and/or actinin, absent evidence to the contrary.

Therefore the disclosure of Carninci et. al. meets the limitations of claims 1,3, 4, 6, 15-18, absent evidence to the contrary.

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RESULT 1
AK043865
LOCUS       AK043865               3185 bp    mRNA    linear   HTC 02-SEP-2005
DEFINITION  Mus musculus 10 days neonate cortex cDNA, RIKEN full-length
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            PROTEIN homolog [Mus musculus], full insert sequence.
ACCESSION   AK043865
VERSION     AK043865.1  GI:26335971
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
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            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium, the RIKEN Genome Exploration Research Group
            Phase I and II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6
  AUTHORS   RIKEN Genome Exploration Research Group, Genome Science Group
            (Genome Network Core Team) and the FANTOM Consortium.
  TITLE     Antisense Transcription in the Mammalian Transcriptome
  JOURNAL   Science 309, 1564-1566 (2005)
REFERENCE   7
  AUTHORS   The FANTOM Consortium, Riken Genome Exploration Research Group and
            Genome Science Group (Genome Network Project Core Group).
  TITLE     The Transcriptional Landscape of the Mammalian Genome
  JOURNAL   Science 309, 1559-1563 (2005)
REFERENCE   8  (bases 1 to 3185)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
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ORIGIN

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Qy          1 CGTAGGAGAGTGACAGGAGCTGTTGTAAGCGTCGCAGCACTGAGCCGCCTCCTCAGGTAT 60
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Qy        181 CTCCCAGCAAGTTCTGTGCTCTTCAGTACCTTTATCCAAAAACGTGCATGGTGTTTTCGG 240
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Qy        241 TGTCTTCTGCACAGGAGAGAACATTGAACAAAGTATTTCCTATCTTGATCAGGAGCTGAC 300
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Qy       601 GAATGAGAAAGATGAGGTACAAAAATTACAAAATATCATAGCCAGCCGGGCTACTCAGTA 660
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Qy       661 TAATCATGATGTGAAGAGGAAGGAGCGTGAATATAATAAGCTAAAGGAGCGCCTGCATCA 720
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Qy       721 GCTCGTTATGAACAAGAAGGATAAAAACATAGCCATGGATGTTTTAAATTATGTGGGTCG 780
Db      1030 GCTCGTTATGAACAAGAAGGATAAAAACATAGCCATGGATGTTTTAAATTATGTGGGTCG 1089

Qy       781 AGCTGATGGCAAACGAGGCTCATGGAGGACTGACAAAACAGAAGCCAGGAATGAAGATGA 840
Db      1090 AGCTGATGGCAAACGAGGCTCATGGAGGACTGACAAAACAGAAGCCAGGAATGAAGATGA 1149

Qy       841 GATGTACAAAATTCTGTTGAATGATTATGAGTACCGCCAGAAGCAGATCCTGATGGAGAA 900
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Qy       901 CGCGGAGCTGAAGAAGGTCCTCCAGCAGATGAAGAAGGAGATGATCTCTCTCCTGTCTCC 960
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Qy       961 TCAGAAGAAGAAGCCCAGGGAAAGAGCAGAGGACGGCACAGGCACTGTTGCTATCTCCGA 1020
Db      1270 TCAGAAGAAGAAGCCCAGGGAAAGAGCAGAGGACGGCACAGGCACTGTTGCTATCTCCGA 1329

Qy      1021 TATAGAAGATGACTCTGGGGAACTGAGCAGAGACAGCGTGTGGGGCCTTTCCTGTGACAC 1080
Db      1330 TATAGAAGATGACTCTGGGGAACTGAGCAGAGACAGCGTGTGGGGCCTTTCCTGTGACAC 1389

Qy      1081 TGTGAGAGAGCAGCTGACAAACAGCATCAGGAAACAGTGGAGAATTTTGAAAAGTCATGT 1140
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Qy      1141 AGAAAAACTCGATAACCAAGCTTCGAAGGTACACTCAGAGGGCCTTAATGAGGAGGACGT 1200
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Qy      1201 CATCTCACGACAAGACCATGAGCAAGAGACTGAGAAACTGGAGCTGGAGATTGAGCGGTG 1260
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Qy      1261 TAAAGAGATGATCAAGGCTCAGCAGCAGCTCTTACAGCAGCAGCTGGCCACCACGTGTGA 1320
Db      1570 TAAAGAGATGATCAAGGCTCAGCAGCAGCTCTTA---CAGCAGCTGGCCACCACGTGTGA 1626

Qy      1321 TGATGACACCACCTCACTGTTGCGAGACTGTTACTTGCTGGAAGAAAAGGAACGCCTTAA 1380
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Qy      1441 TACAGAAGCTGCCATTCGATTGGGGTTGGAGAGAAAGGCGTTTGAAGAAGAGCGAGCCAG 1500
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Db      1867 GAAACTTTTCAGTGCCTTCTCAGGAAGTTCTGATCCAGACAATCTTATAGTCCACTCACG 1926

Qy      1621 GCCACGGCAAAAGAAGCTACACAGTGTGGCTAATGGGGTGCCAGCTTGCACATCAAAACT 1680
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Db      2047 GTCTGAACACAGTTCCATCAGTGTGCTGAATATAACTCCTGAAGAAAGTAAACCAAGTGA 2106

Qy      1801 GGTTGCAAGAGAAAGCACGGATCAGAAGTGGAGCGTGCAGTCGAGGCCCAGCTCGCGGGA 1860
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Db      2107 GGTTGCAAGAGAAAGCACGGATCAGAAGTGGAGCGTGCAGTCGAGGCCCAGCTCGCGGGA 2166

Qy      1861 GGGGTGCTACAGCGGATGCTCCTCGGCCTTCAGGAGCGCTCACGGGGACCGAGATGACTT 1920
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Db      2167 GGGGTGCTACAGCGGATGCTCCTCGGCCTTCAGGAGCGCTCACGGGGACCGAGATGACTT 2226

Qy      1921 ACCTTAAATGTGCGGGCTGCAGTGCTGTTCCCAGATGTGCGCTAGAGGAGTTGACACAGG 1980
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Db      2227 ACCTTAAATGTGCGGGCTGCAGTGCTGTTCCCAGATGTGCGCTAGAGGAGTTGACACAGG 2286

Qy      1981 GTGTAGCATAAAGTCAGTCGTCTAACTTAAGATGCTCAGAGTTGTTTGTTTGGACTTCGC 2040
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Qy      2041 TGTCTTCCCCCAAAGAGCTGAAATGCTAAGCTACTTAAAAGGATGCAAAGCTTTGGTTGT 2100
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Qy       2461 AATGTTTTCAGTGGCATGGTGTTTACAGAGGTTAGGACCACTGCCACATGACAGTTAAGA 2520
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Qy       2521 CTTTATTTTTAAGCCATCTGGGCAATAAAAATTCAAAGCCCCTTCATAAGCTGAGTTCAG 2580
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Db       2947 ATATGTGAATGTTATAATTTCTAAGAGGAATATTGATTATGGAGTAATGGGG 2998
```

14. Claims 1,3, 4, 6, 14-18 are rejected under 35 U.S.C. 102(a) as being anticipated by Mammalian Gene Collection (MGC) Program team (PNAS, Vol. 99, pages 16899-16903), December 24, 2002)

MGC Program team (also see attached sequence comparison) disclose a polynucleotide, which has 99.9% query match and 99.9% identity to the polynucleotide of SEQ ID NO:1. MGC Program team also disclose the polynucleotide encodes a polypeptide that has 100% query match and 100% identity to the polypeptide of SEQ ID NO:2. The disclosed polynucleotide encodes a polypeptide that inherently binds afadin and/or actinin, absent evidence to the contrary.

Further disclosed is vector comprising said polynucleotide and cell comprising said vector. Therefore the disclosure of the MGC Program meets the

limitations of claims 1,3, 4, 6, 14-18, absent evidence to the contrary.

```
RESULT 3
BC021749
LOCUS       BC021749               3425 bp    mRNA    linear   ROD 18-JUL-2005
DEFINITION  Mus musculus synovial sarcoma, X breakpoint 2 interacting protein,
            mRNA (cDNA clone MGC:25823 IMAGE:4165430), complete cds.
ACCESSION   BC021749
VERSION     BC021749.1  GI:18256805
KEYWORDS    MGC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3425)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 3425)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (18-JAN-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
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            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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                     PEESKPSEVARESTDQKWSVQSRPSSREGCYSGCSSAFRSAHGDRDDLP"
ORIGIN

  Query Match           99.9%;  Score 2688.8;  DB 6;  Length 3425;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2690;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CGTAGGAGAGTGACAGGAGCTGTTGTAAGCGTCGCAGCACTGAGCCGCCTCCTCAGGTAT 60
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Qy         61 CCTGGCTCTGGAACTTGCTATGGGAGATTGGATGACTGTGACAGATCCAGTTCTGTGTAC 120
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Qy        481 GCAGAGCTGCTACGCCAAACTTAAGGAGCAGTTGGAAACGTCCAGGCGGGAGATGATCGG 540
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Qy        601 GAATGAGAAAGATGAGGTACAAAAATTACAAAATATCATAGCCAGCCGGGCTACTCAGTA 660
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```

15. No claim is allowed.

16. Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory

period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Advisory

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Nirmal S. Basi whose telephone number is 571-272-0868. The examiner can normally be reached on 9:00 AM-5:30 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Nickol can be reached on 571-272-0835. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

Nirmal S. Basi
Art Unit 1646

GARY B. NICKOL, PH.D.
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

Appendix 1

IFW16

RAW SEQUENCE LISTING DATE: 12/28/2006
PATENT APPLICATION: US/10/644,084A TIME: 18:31:08

Input Set : A:\2144.0100000_E1-X0202-USsq.txt
Output Set: N:\CRF4\12282006\J644084A.raw

see p.6

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 3 <110> APPLICANT: EISAI CO., LTD.
 5 <120> TITLE OF INVENTION: ADIP PROTEIN AND USE THEREOF
 7 <130> FILE REFERENCE: 2144.0100000
 9 <140> CURRENT APPLICATION NUMBER: US 10/644,084A
10 <141> CURRENT FILING DATE: 2003-08-20
12 <150> PRIOR APPLICATION NUMBER: JP 2002-284263
13 <151> PRIOR FILING DATE: 2002-09-27
15 <160> NUMBER OF SEQ ID NOS: 9
17 <170> SOFTWARE: PatentIn version 3.3
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2692
21 <212> TYPE: DNA
22 <213> ORGANISM: Mus musculus
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (80)..(1927)
28 <223> OTHER INFORMATION: /note="afadin-and alpha-actinin-binding protein"
30 <400> SEQUENCE: 1
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33 cctggctctg gaacttgct atg gga gat tgg atg act gtg aca gat cca gtt     112
34                     Met Gly Asp Trp Met Thr Val Thr Asp Pro Val
35                     1               5                  10
37 ctg tgt aca gaa aac aaa aat ctc tct caa tat acc tca gaa aca aag     160
38 Leu Cys Thr Glu Asn Lys Asn Leu Ser Gln Tyr Thr Ser Glu Thr Lys
39             15                  20                  25
41 atg tct ccg tcc agt ttg tac tcc cag caa gtt ctg tgc tct tca gta     208
42 Met Ser Pro Ser Ser Leu Tyr Ser Gln Gln Val Leu Cys Ser Ser Val
43         30                  35                  40
45 cct tta tcc aaa aac gtg cat ggt gtt ttc ggt gtc ttc tgc aca gga     256
46 Pro Leu Ser Lys Asn Val His Gly Val Phe Gly Val Phe Cys Thr Gly
47     45                  50                  55
49 gag aac att gaa caa agt att tcc tat ctt gat cag gag ctg acc acc     304
50 Glu Asn Ile Glu Gln Ser Ile Ser Tyr Leu Asp Gln Glu Leu Thr Thr
51 60                  65                  70                  75
53 ttc ggg ttt cct tcc ttg tat gaa gaa tcc aaa agt aaa gag gca aag     352
54 Phe Gly Phe Pro Ser Leu Tyr Glu Glu Ser Lys Ser Lys Glu Ala Lys
55                 80                  85                  90
57 aga gaa tta aat ata gtc gct gtt ctg aac tgt atg aac gag ctg ctc     400
58 Arg Glu Leu Asn Ile Val Ala Val Leu Asn Cys Met Asn Glu Leu Leu
59             95                  100                 105
61 gtg ctt cag cgg aag aac ctg ctg gcc cag gag agc gtg gag aca cag     448
62 Val Leu Gln Arg Lys Asn Leu Leu Ala Gln Glu Ser Val Glu Thr Gln
63         110                 115                 120
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RAW SEQUENCE LISTING DATE: 12/28/2006
PATENT APPLICATION: US/10/644,084A TIME: 18:31:08

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Output Set: N:\CRF4\12282006\J644084A.raw

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69 aaa ctt aag gag cag ttg gaa acg tcc agg cgg gag atg atc ggg ctt      544
70 Lys Leu Lys Glu Gln Leu Glu Thr Ser Arg Arg Glu Met Ile Gly Leu
71 140                 145                 150                 155
73 caa gag aga gac agg cag ctg cag tgc aag aac agg agt ttg cat cag      592
74 Gln Glu Arg Asp Arg Gln Leu Gln Cys Lys Asn Arg Ser Leu His Gln
75                 160                 165                 170
77 ctc ctg aag aat gag aaa gat gag gta caa aaa tta caa aat atc ata      640
78 Leu Leu Lys Asn Glu Lys Asp Glu Val Gln Lys Leu Gln Asn Ile Ile
79             175                 180                 185
81 gcc agc cgg gct act cag tat aat cat gat gtg aag agg aag gag cgt      688
82 Ala Ser Arg Ala Thr Gln Tyr Asn His Asp Val Lys Arg Lys Glu Arg
83         190                 195                 200
85 gaa tat aat aag cta aag gag cgc ctg cat cag ctc gtt atg aac aag      736
86 Glu Tyr Asn Lys Leu Lys Glu Arg Leu His Gln Leu Val Met Asn Lys
87     205                 210                 215
89 aag gat aaa aac ata gcc atg gat gtt tta aat tat gtg ggt cga gct      784
90 Lys Asp Lys Asn Ile Ala Met Asp Val Leu Asn Tyr Val Gly Arg Ala
91 220                 225                 230                 235
93 gat ggc aaa cga ggc tca tgg agg act gac aaa aca gaa gcc agg aat      832
94 Asp Gly Lys Arg Gly Ser Trp Arg Thr Asp Lys Thr Glu Ala Arg Asn
95                 240                 245                 250
97 gaa gat gag atg tac aaa att ctg ttg aat gat tat gag tac cgc cag      880
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99             255                 260                 265
101 aag cag atc ctg atg gag aac gcg gag ctg aag aag gtc ctc cag cag      928
102 Lys Gln Ile Leu Met Glu Asn Ala Glu Leu Lys Lys Val Leu Gln Gln
103         270                 275                 280
105 atg aag aag gag atg atc tct ctc ctg tct cct cag aag aag aag ccc      976
106 Met Lys Lys Glu Met Ile Ser Leu Leu Ser Pro Gln Lys Lys Lys Pro
107     285                 290                 295
109 agg gaa aga gca gag gac ggc aca ggc act gtt gct atc tcc gat ata     1024
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111 300                 305                 310                 315
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123         350                 355                 360
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126 Val His Ser Glu Gly Leu Asn Glu Glu Asp Val Ile Ser Arg Gln Asp
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PATENT APPLICATION: US/10/644,084A TIME: 18:31:08

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134 Glu Met Ile Lys Ala Gln Gln Gln Leu Leu Gln Gln Gln Leu Ala Thr
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147     445                 450                 455
149 cga ttg ggg ttg gag aga aag gcg ttt gaa gaa gag cga gcc agc tgg    1504
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153 gta aag cag cag ttt tta aac atg acg aac ttt gac cac cag aac tca    1552
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155                 480                 485                 490
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162 Asn Leu Ile Val His Ser Arg Pro Arg Gln Lys Lys Leu His Ser Val
163         510                 515                 520
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167     525                 530                 535
169 gcc tca cct tct act tca gac ttt cgc cag aca cat tca tgt gtg tct    1744
170 Ala Ser Pro Ser Thr Ser Asp Phe Arg Gln Thr His Ser Cys Val Ser
171 540                 545                 550                 555
173 gaa cac agt tcc atc agt gtg ctg aat ata act cct gaa gaa agt aaa    1792
174 Glu His Ser Ser Ile Ser Val Leu Asn Ile Thr Pro Glu Glu Ser Lys
175                 560                 565                 570
177 cca agt gag gtt gca aga gaa agc acg gat cag aag tgg agc gtg cag    1840
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182 Ser Arg Pro Ser Ser Arg Glu Gly Cys Tyr Ser Gly Cys Ser Ser Ala
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185 ttc agg agc gct cac ggg gac cga gat gac tta cct taa atgtgcgggc      1937
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231 Leu Tyr Ser Gln Gln Val Leu Cys Ser Ser Val Pro Leu Ser Lys Asn
232 35 40 45
235 Val His Gly Val Phe Gly Val Phe Cys Thr Gly Glu Asn Ile Glu Gln
236 50 55 60
239 Ser Ile Ser Tyr Leu Asp Gln Glu Leu Thr Thr Phe Gly Phe Pro Ser
240 65 70 75 80
243 Leu Tyr Glu Glu Ser Lys Ser Lys Glu Ala Lys Arg Glu Leu Asn Ile
244 85 90 95
247 Val Ala Val Leu Asn Cys Met Asn Glu Leu Leu Val Leu Gln Arg Lys
248 100 105 110
251 Asn Leu Leu Ala Gln Glu Ser Val Glu Thr Gln Asn Leu Lys Leu Gly
252 115 120 125
255 Ser Asp Met Asp His Leu Gln Ser Cys Tyr Ala Lys Leu Lys Glu Gln
256 130 135 140
259 Leu Glu Thr Ser Arg Arg Glu Met Ile Gly Leu Gln Glu Arg Asp Arg
260 145 150 155 160
263 Gln Leu Gln Cys Lys Asn Arg Ser Leu His Gln Leu Leu Lys Asn Glu
264 165 170 175
267 Lys Asp Glu Val Gln Lys Leu Gln Asn Ile Ile Ala Ser Arg Ala Thr
268 180 185 190
271 Gln Tyr Asn His Asp Val Lys Arg Lys Glu Arg Glu Tyr Asn Lys Leu
272 195 200 205
275 Lys Glu Arg Leu His Gln Leu Val Met Asn Lys Lys Asp Lys Asn Ile
276 210 215 220
279 Ala Met Asp Val Leu Asn Tyr Val Gly Arg Ala Asp Gly Lys Arg Gly
280 225 230 235 240
283 Ser Trp Arg Thr Asp Lys Thr Glu Ala Arg Asn Glu Asp Glu Met Tyr
284 245 250 255
287 Lys Ile Leu Leu Asn Asp Tyr Glu Tyr Arg Gln Lys Gln Ile Leu Met
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RAW SEQUENCE LISTING DATE: 12/28/2006
PATENT APPLICATION: US/10/644,084A TIME: 18:31:08

Input Set : A:\2144.0100000_E1-X0202-USsq.txt
Output Set: N:\CRF4\12282006\J644084A.raw

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303 Glu Leu Ser Arg Asp Ser Val Trp Gly Leu Ser Cys Asp Thr Val Arg
304                 325                 330                 335
307 Glu Gln Leu Thr Asn Ser Ile Arg Lys Gln Trp Arg Ile Leu Lys Ser
308             340                 345                 350
311 His Val Glu Lys Leu Asp Asn Gln Ala Ser Lys Val His Ser Glu Gly
312         355                 360                 365
315 Leu Asn Glu Glu Asp Val Ile Ser Arg Gln Asp His Glu Gln Glu Thr
316     370                 375                 380
319 Glu Lys Leu Glu Leu Glu Ile Glu Arg Cys Lys Glu Met Ile Lys Ala
320 385                 390                 395                 400
323 Gln Gln Gln Leu Leu Gln Gln Gln Leu Ala Thr Thr Cys Asp Asp Asp
324                 405                 410                 415
327 Thr Thr Ser Leu Leu Arg Asp Cys Tyr Leu Leu Glu Glu Lys Glu Arg
328             420                 425                 430
331 Leu Lys Glu Glu Trp Thr Leu Phe Lys Glu Gln Lys Lys Asn Phe Glu
332         435                 440                 445
335 Arg Glu Arg Arg Ser Phe Thr Glu Ala Ala Ile Arg Leu Gly Leu Glu
336     450                 455                 460
339 Arg Lys Ala Phe Glu Glu Glu Arg Ala Ser Trp Val Lys Gln Gln Phe
340 465                 470                 475                 480
343 Leu Asn Met Thr Asn Phe Asp His Gln Asn Ser Glu Asn Val Lys Leu
344                 485                 490                 495
347 Phe Ser Ala Phe Ser Gly Ser Ser Asp Pro Asp Asn Leu Ile Val His
348             500                 505                 510
351 Ser Arg Pro Arg Gln Lys Lys Leu His Ser Val Ala Asn Gly Val Pro
352         515                 520                 525
355 Ala Cys Thr Ser Lys Leu Thr Lys Ser Leu Pro Ala Ser Pro Ser Thr
356     530                 535                 540
359 Ser Asp Phe Arg Gln Thr His Ser Cys Val Ser Glu His Ser Ser Ile
360 545                 550                 555                 560
363 Ser Val Leu Asn Ile Thr Pro Glu Glu Ser Lys Pro Ser Glu Val Ala
364                 565                 570                 575
367 Arg Glu Ser Thr Asp Gln Lys Trp Ser Val Gln Ser Arg Pro Ser Ser
368             580                 585                 590
371 Arg Glu Gly Cys Tyr Ser Gly Cys Ser Ser Ala Phe Arg Ser Ala His
372         595                 600                 605
375 Gly Asp Arg Asp Asp Leu Pro
376     610                 615
379 <210> SEQ ID NO: 3
380 <211> LENGTH: 3195
381 <212> TYPE: DNA
382 <213> ORGANISM: Rattus norvegicus
385 <220> FEATURE:
386 <221> NAME/KEY: CDS
387 <222> LOCATION: (79)..(1920)
```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 12/28/2006
PATENT APPLICATION: US/10/644,084A TIME: 18:31:09

Input Set : A:\2144.0100000_E1-X0202-USsq.txt
Output Set: N:\CRF4\12282006\J644084A.raw

FYI

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 2422

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8

VERIFICATION SUMMARY DATE: 12/28/2006
PATENT APPLICATION: US/10/644,084A TIME: 18:31:09

Input Set : A:\2144.0100000_E1-X0202-USsq.txt
Output Set: N:\CRF4\12282006\J644084A.raw

L:569 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2420